BISS Biodiversity Information Science and Standards

Biodiversity Information Science and Standards 3: e38493
doi: 10.3897/biss.3.38493

OPEN ACCESS

Conference Abstract

SYNTHESYS+ Molecular Collections in the Age of Genomics: Standards and processes

Ole Seberg[‡], Gabriele Droege[§], Jonas J Astrin[|], Katharine Barker[¶], Jonathan Coddington[¶]

‡ Natural History Museum of Denmark, University of Copenhagen, Copenhagen, Denmark
§ Botanic Garden and Botanical Museum Berlin, Berlin, Germany
| ZFMK, Bonn, Germany
¶ National Museum of Natural History, Smithsonian Institution, Washington, D.C., United States of America

Corresponding author: Ole Seberg (oles@snm.ku.dk), Gabriele Droege (g.droege@bgbm.org), Jonas J Astrin (j.astrin.zfmk@uni-bonn.de), Katharine Barker (barkerk@si.edu), Jonathan Coddington (coddington@si.edu)

Received: 24 Jul 2019 | Published: 30 Jul 2019

Citation: Seberg O, Droege G, Astrin JJ, Barker K, Coddington J (2019) SYNTHESYS+ Molecular Collections in the Age of Genomics: Standards and processes. Biodiversity Information Science and Standards 3: e38493. https://doi.org/10.3897/biss.3.38493

Abstract

The aim of the Global Genome Biodiversity Network (GGBN, http://www.ggbn.org) is to foster collaboration among biodiversity biobanks on a global scale in order to further compliance with standards, best practices, and to secure interoperability and exchange of material in accordance with national and international legislation and conventions. Thus, key aspects of GGBN's mission are to develop a network of trusted collections, establishing standards, and identifying best practices by reaching out to other communities. This is especially critical in the light of new international legislation such as the recent Nagoya Protocol on Access and Benefit Sharing (ABS).

Biological repositories such as but not limited to natural history collections, botanic gardens, culture collections and zoos are facing a series of challenges triggered by the rapid acceleration in sequencing technology that has put added pressure on the use of samples, which just a few years ago were considered inaccessible for sequencing.

ABS legislation applies to nearly all collection types, and with biodiversity biobanks increasing in number worldwide, there is an urgent need to streamline procedures and to ensure legislative compliance. Within Europe it is necessary to 1) reach common

© Seberg O et al. This is an open access article distributed under the terms of the Creative Commons Attribution License (CC BY 4.0), which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.

standards for biodiversity and environmental biobanks; 2) define best practices for the use of molecular collections; and 3) try to ease exchange of samples and related information, while staying compliant with legislation and conventions.

Within the EU funded SYNTHESYS+ project (http://www.synthesys.info), GGBN is leading Network Activity 3 (NA3). An overview of planned activities and tasks will be given here with special emphasis on linkages within and beyond SYNTHESYS+.

Presenting author

Ole Seberg

Presented at

Biodiversity_Next 2019